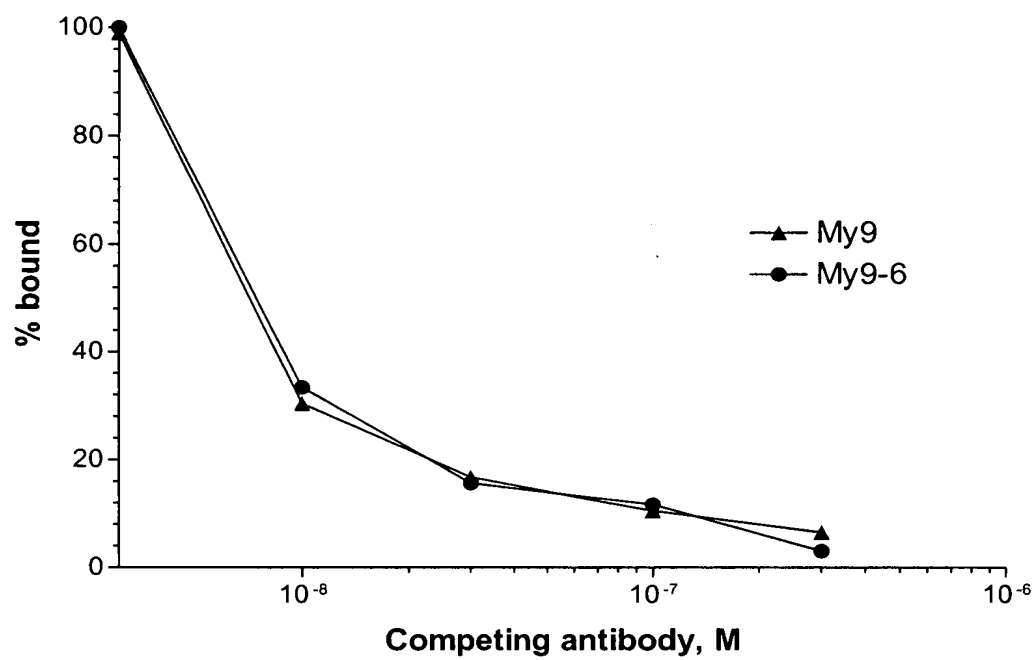


Attorney Docket No. A8427

Figure 1



Attorney Docket No. A8427

Figure 2

My9-6 Light Chain Signal Sequence Degenerate Primers

<u>Name</u>	<u>Sequence</u>	<u>SEQ ID NO:</u>
Leaddeg1	TTTTGATTCTGCTGTGGGTGTCCGGNACNTGYGG	17
Leaddeg2	TTTTGATTTCGCTGCTGCTGCTGTGGGTNWSNGG	18
Leaddeg3	TTTTGATTCCCAGGTGTTTCATGCTGCTGYTNYTNTGGGT	19

Mixed bases: S = G+C, Y = C+T, W = A+T, N = A+T+G+C.

Figure 3

127 Brookhaven Structure Files Used for Surface Predictions									
2rcs	3hfl	3hfm	1aif	1a3r	1bbj	43c9	4fab	6fab	7fab
2gfb	2h1p	2hfl	1a6t	1axt	1bog	2hrp	2jel	2mcp	2pcp
1yuh	2bfv	2cgr	8fab	1ae6	1bvl	2dbl	2f19	2fb4	2fbj
1sm3	1tet	1vfa	glb2	1a4j	1cly	1vge	1yec	1yed	1yee
1nsn	1opg	1osp	1aj7	1ay1	1clz	1plg	1psk	1rmf	1sbs
1ncd	1nfd	1ngp	1acy	1afv	1cbv	1nld	1nma	1nmb	1nqb
1mcp	1mfb	1mim	15c8	1a5f	1axs	1mLb	1mpa	1nbv	1ncb
1jrh	1kb5	1kel	1ap2	1b2w	1adq	1kip	1kir	1lve	1mam
1igi	1igm	1igt	1ad0	1baf	1cfv	1igy	1ikf	1jel	1jhl
1gpo	1hil	1hyx	1a0q	1bjm	1clo	1iai	1ibg	1igc	1igf
1fpt	1frg	1fvc	1aqk	1bln	1d5b	1gaf	1ggi	1ghf	1gig
1fai	1fbi	1fdl	1ad9	1bbd	1f58	1fgv	1fig	1flr	1for
	1dbl	1dfb	1a3l	1bfo	1eap	1dsf	1dvf		

Figure 4

Primer	Sequence	SEQ ID NO:
My96LCBsrG1	TACAGGTGTACACTCCGATATTGTGATCACCCAGACTCC	20
My96LCOL1	ACTGGAATCAAACGAACGTGGCTGCACCATCTG	21
My96LCOL2	GCCACAGTTCGTTTGATTCCAGTTGGTGCCTCC	22
My96HCBsrG1	TACAGGTGTACACTCCAGGTTAAGCTGCAGCAGTCTGG	23
My96HCOL1	CCACGGTCACCGTCTCCTCAGCCTCCACC	24
My96HCOL2	GAGGCTGAGGAGACGGTGACCGTGGTCCC	25
My9-6LCNMLS	CAGGTGTACACTCCAATATTATGCTCACCCAGAGTCCATCATC	26
My9-6HCQP	CAGGTGTACACTCCCAGGTTCAAGTGCAGCAGCCTGGGGCTG	27
MY96HCQ64-1	AGAAGTTCCAAGGCAAGGCCAC	28
MY96HCQ64-2	CTTGCCCTTGGAACTTCTGATTG	29
MY96HCQ105	CGATGGGCCCTTGGTGAGGCTGAGGAGACGGTGACCGTGGTCCCCTTGGCCCCAGACATC	30
MY96LCEVGPR	AGGTGTACACTCCGAGATTGTGCTACCCAGAGTCCAGGATCTCTGGCTGTGTCTCCAGGAGAAAGGGTCACTATGAGC	31
MY96LCR45	GCCTGGTACCAACAGATACCAAGGCGAGTCTCCTAGACTTCTGATCTAC	32
MY96LCP80-1	AGCAGTGTTCACCTGAAGACCTGGC	33
MY96LCP80-2	GTCTTCAGGTTGAACACTGCTGATGG	34
MY96LCQ100	TTTTAAGCTTCGTTTGATTCCAGTTTGGTGGCCTTGACCCGAACGTCCG	35
My96lcNM	CAGGTGTACACTCCAATATTATGCTCACCCAGAG	36
MY96LCK45	GCCTGGTACCAACAGATACCAAGGCGAGTCTCCTAAACTTCTGATCTAC	37
My96HCAPal	CGATGGGCCCTTGGTGAGGCTGAGGAGACGGTGACCCG	38
huMy96LCOL1	ACTGGAATCAAACGTACGGTGGCTGCACCATCTG	39
huMy96LCOL2	GCCACCGTACGTTTGATTTCAGTTTGGTGGCCTTG	40
My96lcEM	CAGGTGTACACTCCGAGATTATGCTCACCCAGAG	41
My96lcNV	CAGGTGTACACTCCAATATTGTGCTCACCCAGAG	42
chMy96lcBsiW1	TTTTTCGTACGTTTGATTTCAGTTTCCAGTTTGGTGCC	43

Figure 5

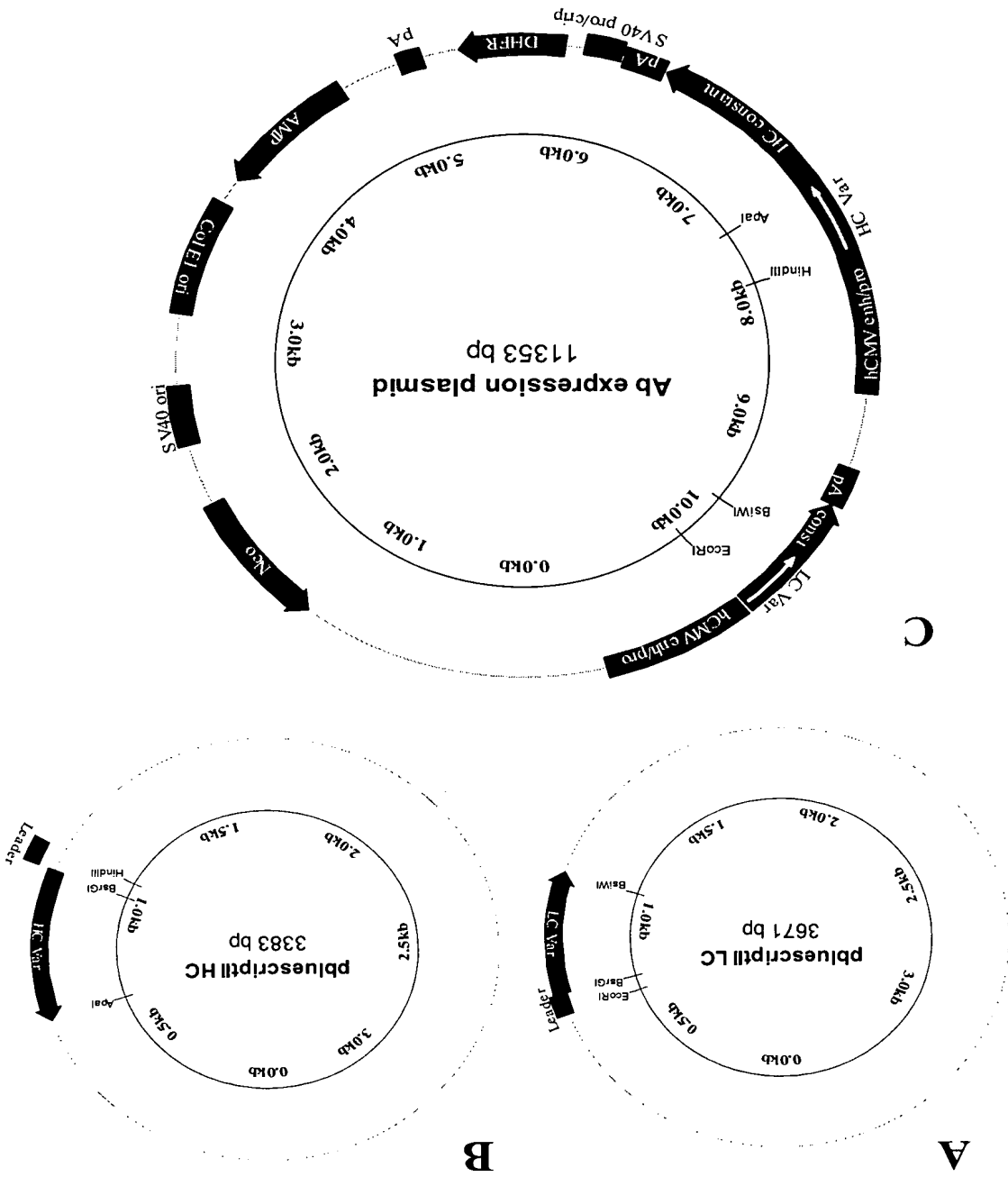


Figure 6A

muMy9-6 Light Chain Amino Terminal Peptide Sequence										SEQ ID NO:														
Edman Sequence	Kabat#	5 10 15 20 23								44														
		N	I	M	L	T	Q	S	P	S	S	L	A	V	S	A	G	E	K	V	T	M	(S)	X
Deg cDNA		D	I	V	I	T	Q	T	P	S	S	L	A	V	S	A	G	E	K	V	T	M	S	C
SacIMK Primer	E L D I V X T Q X X GG GAG CTC GAY ATT GTG MTS ACM CAR WCT MCA																							46
Signal Pep Deg cDNA		N	I	M	L	T	Q	S	P	S	S	L	A	V	S	A	G	E	K	V	T	M	S	C
																								47

Figure 6B

MS-MS Sequence Analysis of muMy9-6 Light Chain CDR Peptide Fragments										SEQ ID NO:
CDR1	K S S Q S V F F S S S Q K N Y L A									48
1319 Da	S S Q S V F F S S S Q K									49
CDR2	K L L I Y W A S T R E S									50
1122 Da	K L L I Y W A S T R E									51

Figure 7

muMy9-6 Heavy Chain Internal/CDR3 Peptide Sequence		SEQ ID NO:
1788 Da Sequence	(R) Y F D V W G A G T T V T V S S A K (T)	52
cDNA clone 2 (match)	<div> <div>CDR3</div> <div> <div>E V R L R Y F D V</div> <div>W G A G T T V T V S S</div> </div> </div>	53
cDNA clone 1 (no match)	<div> <div>CDR3</div> <div> <div>M G E D A - M D Y W G Q G T S V T V S S</div> </div> </div>	54

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Figure 8A

Light Chain (sequential numbering) (SEQ ID NO:55):

```
1 aacattatgctgacacagtcgccatcatctctggctgtgtctgca
1  N I M L T Q S P S S L A V S A

46 ggagaaaaggctcactatgagctgtaagtccagtc aaagtgttttt
16  G E K V T M S C K S S Q S V F
                               CDR1

91 ttcagttcaagtcagaagaactacttggcctggtaccaacagata
31  F S S S Q K N Y L A W Y Q Q I
                               CDR1

136 ccagggcagtcctcctaaacttctgatctactgggcatccactagg
46  P G Q S P K L L I Y W A S T R
                               CDR2

181 gaatctggtgtccctgatcgcttcacaggcagtg gatctgggaca
61  E S G V P D R F T G S G S G T

226 gattttactcttaccatcagcagtg tacaatctgaagacctggca
76  D F T L T I S S V Q S E D L A

271 atttattactgtcatcaatacctctcctcgcgacgttcggtgga
91  I Y Y C H Q Y L S S R T F G G
                               CDR3

316 ggcaccaaactggaaatcaaacga
106 G T K L E I K R
```

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Figure 8B

Heavy Chain (sequential numbering) (SEQ ID NO:56):

```
1 caggtgcaactgcagcagcctggggctgaggtggtgaagcctggg
1 Q V Q L Q Q P G A E V V K P G

46 gcctcagtgaagatgtcctgcaaggcttctggctacacatttacc
16 A S V K M S C K A S G Y T F T

91 agttactatatacactggataaagcagacacctggacagggcctg
31 S Y Y I H W I K Q T P G Q G L
    CDR1

136 gaatggggttgaggttatttatccaggaaatgatgatatttcctac
46 E W V G V I Y P G N D D I S Y
    CDR2

181 aatcagaagttcaaaggcaaggccacattgactgcagacaaatcc
61 N Q K F K G K A T L T A D K S
    CDR2

226 tccaccacagcctacatgcaactcagcagcctgacatctgaggac
76 S T T A Y M Q L S S L T S E D

271 tctgcggtctattactgtgcaagagaggttcgtctacggtacttc
91 S A V Y Y C A R E V R L R Y F
    CDR3

316 gatgtctggggcgcagggaccacgggtcaccgtctcctca
106 D V W G A G T T V T V S S
```


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Figure 9

Murine My9-6 CDRs

<u>Light Chain</u>	<u>SEQ ID NO:</u>
CDR1: K S S Q S V F F S S S Q K N Y L A	4
CDR2: W A S T R E S	5
CDR3: H Q Y L S S R T	6
 <u>Heavy Chain</u>	
CDR1: S Y Y I H	1
CDR2: V I Y P G N D D I S Y N Q K F K G	57
CDR3: E V R L R Y F D V	3
 <u>AbM Heavy Chain</u>	
CDR1: G Y T F T S Y Y I H	58
CDR2: V I Y P G N D D I S	59
CDR3: E V R L R Y F D V	3

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Figure 10

GermLine Sequence Comparisons

<u>Light Chain</u>		50
8-27*	NIMMTQSPSSLAVSAGEKVTMSCKSSQSVLYSSNQKNYLAWYQQKPGQSP	
muMy9-6	...L.....FF..S.....I.....	

		99
8-27	KLLIYWASTRESGVPDRFTGSGSGTDFTLTISVQAEDLAVYYCHQYLS	
muMy9-6S.....I.....	

<u>Heavy Chain</u>		50
V102#	-VQLQQPGAELVKPGASVKVSCASGYTFTSYWMHWVKQRPGQGLEWIGR	
muMy9-6	Q.....V.....M.....YI..I..T.....V.V	

		98
V102	IHPSDSDTNYNQKFKGKATLTVDKSSSTAYMQLSSLTSEDSAVYYCA-	
muMy9-6	.Y.GND.IS.....A....T.....R	

* SEQ ID NO:60

SEQ ID NO:61

Sequential residue numbering

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Figure 11A

Light Chain Ten Most Homologous Sequences with Structures

	1					50
My96	NIMLTQSPSS	LAVSAGEKVT	MSCKSSQSVF	FSSSQKNYLA	WYQQIPGQSP	
1sbs	DIVMSQSPSS	LAVSVGEKVT	MTCKSSQSL	YSSNQMNLYA	WYQQKPGQSP	
1hil	DIVMTQSPSS	LTVTAGEKVT	MSCTSSQSLF	NSGKQKNYLT	WYQQKPGQPP	
1a5f	DIVMTQSPSS	LTVTTGEKVT	MTCKSSQSL	NSGAQKNYLT	WYQQKPGQSP	
1a3r	DIVMTQSPSS	LTVTTGEKVT	MTCKSSQSL	NSRTQKNYLT	WYQQKPGQSP	
1frg	DIVMTQSPSS	LTVTAGEKVT	MSCKSSQSLF	NSGKRKNFLT	WYHQKPGQPP	
1mcp	DIVMTQSPSS	LSVSAGERVT	MSCKSSQSL	NSGNQKNFLA	WYQQKPGQPP	
43c9	DVVMQTTPSS	LAMSVGQKVT	MSCKSSQSL	NISNQKNYLA	WYQQKPGQSP	
1lve	DIVMTQSPDS	LAVSLGERAT	INCKSSQSVL	YSSNSKNYLA	WYQQKPGQPP	
1ap2	DIVMTQSPSS	LTVTAGEKVT	MSCKSSQSL	NSGNQKNYLT	WYQQKPGQPP	
1ncb	DIVMTQSPKF	MSTSVGDRV	ITCKASQDVS	T.....AVV	WYQQKPGQSP	
						100
My96	KLLIYWASTR	ESGVPDRFTG	SGSGTDFTLT	ISSVQSEDLA	IYYCHQYLSS	
1sbs	KLLIYWASTR	ESGVPDRFTG	SGSGTDFTLT	ISSVEAEDLA	VYYCQYHSY	
1hil	KVLIYWASTR	ESGVPDRFTG	SGSGTDFTLT	ISSVQAEDLA	VYYCQNDYSN	
1a5f	KLLIYWASTR	ESGVPDRFTG	SGSGTDFTLS	ISGVQAEDLA	VYYCQNNYNY	
1a3r	KLLIYWASTR	ESGVPDRFTG	SGSGTDFTLS	ISGVQAEDLA	VYYCQNNYNY	
1frg	KLLIYWASTR	ESGVPDRFSG	SGSGTDFTLT	ITSVQAEDLA	IYYCQNDYSH	
1mcp	KLLIYGASTR	ESGVPDRFTG	SGSGTDFTLT	ISSVQAEDLA	VYYCQNDHSY	
43c9	KLLVYFASTR	ESGVPDRFIG	SGSGTDFTLT	ISSVQAEDQA	DYFCQQHYRA	
1lve	KLLIYWASTR	ESGVPDRFSG	SGSGTDFTLT	ISSLQAEDVA	VYYCQYYST	
1ap2	KLLIYWASTR	ESGVPDRFTG	SGSGTDFTLT	ISSVQAEDLA	VYYCQNDYSY	
1ncb	KLLIYWASTR	HIGVPDRFAG	SGSGTDYTLT	ISSVQAEDLA	LYYCQQHYSP	
						115
My96	.RTFGGGTKL	EIKRA	(SEQ ID NO:62)			
1sbs	PFTFGSGTKL	EIKRA	(SEQ ID NO:63)			
1hil	PLTFGGGTKL	ELKRA	(SEQ ID NO:64)			
1a5f	PLTFGAGTKL	ELKRA	(SEQ ID NO:65)			
1a3r	PLTFGAGTKL	ELKRA	(SEQ ID NO:66)			
1frg	PLTFGAGTKL	ELKRA	(SEQ ID NO:67)			
1mcp	PLTFGAGTKL	EIKRA	(SEQ ID NO:68)			
43c9	PRTFGGGTKL	EIK	(SEQ ID NO:69)			
1lve	PYSFGQGTKL	EIKR	(SEQ ID NO:70)			
1ap2	PLTFGAGTKL	EPG	(SEQ ID NO:71)			
1ncb	PWTFGGGTKL	EIKRA	(SEQ ID NO:72)			

Residue numbering is sequential

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Figure 11B

Heavy Chain Ten Most Homologous Sequences with Structures

	1				50
My96	QVQLQQPGAE	VVKPGASVKM	SCKASGYTFT	SYYIHWIKQT	PGQGLEWVGV
1plg	QIQLQQSGPE	LVRPGASVKI	SCKASGYTFT	DYYIHWVKQR	PGEGLEWIGW
1ae6	QIQLQQSGPE	LVKPGASVKI	SCKASGYTFT	DYYINWMKQK	PGQGLEWIGW
1for	QGQLQQSGAE	LVRPGSSVKI	SCKASGYAFS	SFWVNWVKQR	PGQGLEWIGQ
1igy	.VKLQESGAE	LARPGASVKM	SCKASGYTFT	TYTIHWIKQR	PGQGLEWIGY
1bbj	XVQLQQSDAE	LVKPGASVKI	SCKASGYTFT	DHAIHWAKQK	PEQGLEWIGY
1nqb	.VQLQQSGAE	LVKPGASVKL	SCKASGYTFT	SYWMHWVKQR	PGRGLEWIGR
1mim	..QLQQSGTV	LARPGASVKM	SCKASGYSFT	RYWMHWIKQR	PGQGLEWIGA
1a6t	EVQLQQSGPD	LVKPGASVKI	SCKASGYSFS	TYWMHWVKQS	HGKSLEWIGR
1d5b	QVQLQQSGAE	LMKPGASVKI	SCKATGYTFS	SFWIEWVKQR	PGHGLEWIGE
1fai	QVQLQQSGAE	LVRAGSSVKM	SCKASGYTFT	SYGVNWVKQR	PGQGLEWIGY
					100
My96	IYPGNDDISY	NQKFKGKATL	TADKSSTTAY	MQLSSLTSED	SAVYYCAREV
1plg	IYPGSGNTKY	NEKFKGKATL	TVDTSSSTAY	MQLSSLTSED	SAVYFCARGG
1ae6	IDPGSGNTKY	NEKFKGKATL	TVDTSSSTAY	MQLSSLTSED	TAVYFCAREK
1for	IYPGDGDNKY	NGKFKGKATL	TADKSSTTAY	MQLYSLTSED	SAVYFCARSG
1igy	INPSSVYTNY	NQRFKDKATL	TRDRSSNTAN	IHLSSLTSDD	SAVYYCVREG
1bbj	ISPGNDDIKY	NEKFKGKATL	TADKSSSTAY	MQLNSLTSED	SAVYFCKRSY
1nqb	IDPNSGGTKY	NEKFKSKATL	TVDKPSSTAY	MQLSSLTSED	SAVYYCARYD
1mim	IYPGNSDTSY	NQKFEGKAKL	TAVTSASTAY	MELSSLTHED	SAVYYCSRDY
1a6t	VDPDNGGTSF	NQKFKGKAIL	TVDKSSSTAY	MELGSLTSED	SAVYYCARRD
1d5b	ILPGSGGTHY	NEKFKGKATF	TADKSSNTAY	MQLSSLTSED	SAVYYCARGH
1fai	INPGKGYLSY	NEKFKGKTTL	TVDRSSSTAY	MQLRSLTSED	AAVYFCARSF
					124
My96	RLRY.....	FDVWGAGTTV	TVSS	(SEQ ID NO:73)	
1plg	K.....FA	MDYWGQGTSV	TVSS	(SEQ ID NO:74)	
1ae6	TTY.....YA	MDYWGQGTSV	TVSS	(SEQ ID NO:75)	
1for	NYPY.....A	MDYWGQGTSV	TVSS	(SEQ ID NO:76)	
1igyE	VPYWGQGTTV	TVSS	(SEQ ID NO:77)	
1bbj	YGHW.....GQGTTL	TVSS	(SEQ ID NO:78)	
1nqb	YYGS....SY	FDYWGQGTTV	TVSS	(SEQ ID NO:79)	
1mim	GYFY.....	.DFWGQGTTL	TVSS	(SEQ ID NO:80)	
1a6t	DY.....Y	FDFWGQGTSV	TVSS	(SEQ ID NO:81)	
1d5b	SYIFY.....D	GDYWGQGTSV	TVSS	(SEQ ID NO:82)	
1fai	YGGSDLAVYY	FDSWGQGTTL	TVSS	(SEQ ID NO:83)	

Residue numbering is sequential

Attorney Docket No. A8427

Figure 12A

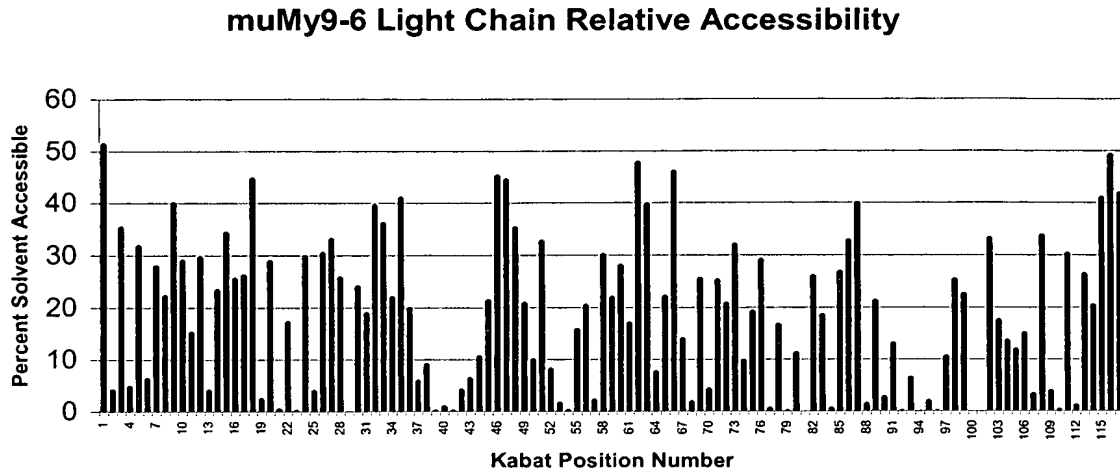
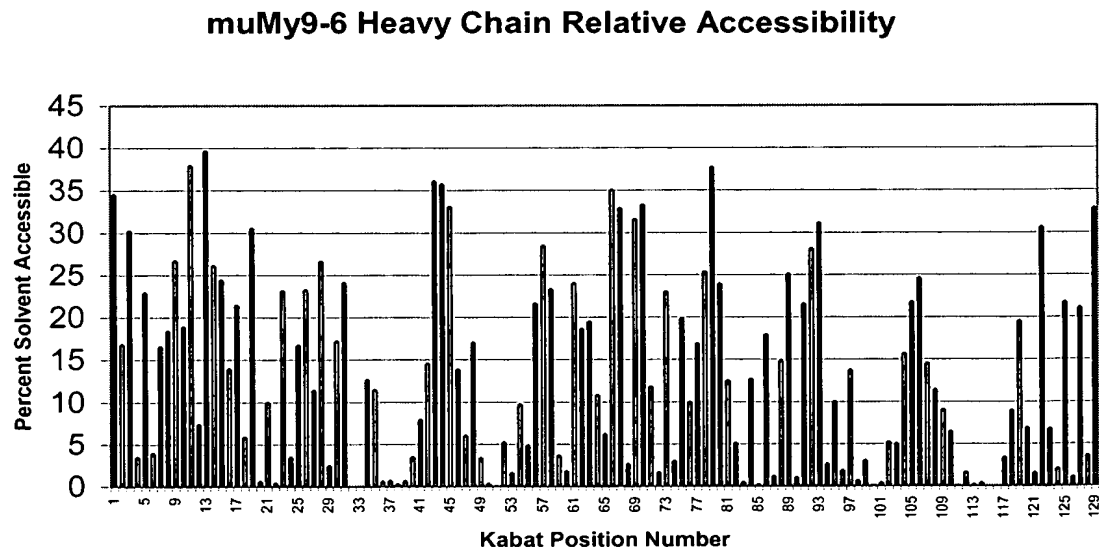


Figure 12B



Attorney Docket No. A8427

Figure 13A

muMy9-6 Light Chain Surface Residues						
Kabat Position #	Average accessibility	> 30% Ave acc	25%-35% Ave acc	Identical flank		muMy9-6 surface
1	51.46	1				N1
3	35.42	3				M3
5	31.82	5	5	NA		T5
7	28.04		7	26.17		
9	40.08	9				S9
10	29.04		10	27.76		
12	29.63		12	22.32	other A's	
15	34.39	15	15	18.20	33.36	A15
16	25.61		16	NA		
17	26.21		17	25.11		
18	44.83	18				K18
20	28.91		20	29.11		
40	45.25	40				P40
41	44.52	41				G41
42	35.34	42				Q42
45	32.68	45	45	32.58		K45
57	39.81	57				G57
60	46.07	60				D60
63	25.60		63	26.87		
65	25.28		65	24.07		
67	32.05	67	67		11ve left out	S67
70	29.16		70	29.28	30.13	D70
76	26.02		76	24.29		
79	26.83		79	NA		
80	32.78	80	80	NA		S80
81	39.95	81				E81
100	33.79	100	100	34.05		G100
103	30.30	103	103	30.30		K103
105	26.42		105	26.96		
107	41.06	107				K107
108	49.29	108				R108
109	41.85	109				A109

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Figure 13B

muMy9-6 Heavy Chain Surface Residues					
Kabat Position #	Average accessibility	> 30% Ave accessibility	25%-35% Ave acc	Identical flank	muMy9-6 surface
1	40.08	1			Q1
3	38.62	3			Q3
5	28.06		5	NA	
9	35.98	9			A9
11	48.07	11			V11
13	49.75	13			K13
14	32.39	14	14	32.20	P14
15	30.69	15	15	31.84	G15
17	26.01		17	26.67	
19	37.64	19			K19
23	29.92		23	30.11	K23
26	29.48		26	31.43	G26
28	33.67	28	28	35.59	T28
41	44.46	41			P41
42	46.28	42			G42
43	42.00	43			Q43
52B	25.21		52B	25.21	
53	28.84		53	28.84	
56	29.08		56	29.08	
61	43.12	61			Q61
62	44.46	62			K62
64	38.56	64			K64
65	41.85	65			G65
68	28.38		68	28.30	
70	25.14		70	28.21	
73	32.97	73	73	35.71	K73
74	47.68	74			S74
75	26.67		75	27.22	
82B	32.62	82B	82B	30.58	S82B
83	26.03		83	26.52	
84	35.34	84			S84
85	37.78	85			E85
105	36.29	105			A105
108	25.74		108	28.73	
110	26.94		110	23.38	
112	41.61	112			S112

Figure 14

muMy9-6 Surface Residues
within 5 Å of a CDR Residue

Light chain	Heavy chain
N1	Q1
M3	T28
T5	K64
K45	K73
G57	
D60	
S67	
D70	

Figure 15

Top Five Most Homologous Human Antibody Surfaces					
Antibody	Light Chain		SEQ ID NO:	Heavy Chain	SEQ ID NO:
muMy9-6	N M T S A K P G Q K G D S D S E G K K R A		84	Q Q A V K P G K G T P G Q Q K K G K S S E A S	90
2IH9	D Q T S V R P G E K G S S D P E G K K R T		85	Q Q A V K P G K G T P G Q Q K Q G T P S S E K S	91
EL-14	D V T S V R P G K K G S S D P E G K K R -		86	Q Q A A K P G K G T P G Q Q K Q G G S S E Q S	92
CLL-412	D Q T S V R P G K K G S S D P E Q K K R T		87	Q Q A V K P G K G T P G Q Q K Q G T S S S E Q S	93
LC3bPB	E V T G P R P G Q R G D S D P E Q K K R -		88	- Q A V K P G K G T P G Q Q K Q G K S S E Q S	94
CLL1.69	D V T L L P P G Q R G D A D A E Q K K R -		89	Q Q A V K P G K G T P G Q Q K Q G K S S E Q S	95

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Figure 16A

Humanized My9-6 Light Chain Versions

Kabat #	10	20	27b	34	44
muMy9-6	NIMLTQSPSS	LAVSAGEKVT	MSCKSSQSVF	FSSSQKNYLA	WYQQIPGQSP
huMy9-6 V1.0	EIVLTQSPGS	LAVSPGERVT	MSCKSSQSVF	FSSSQKNYLA	WYQQIPGQSP
huMy9-6 V1.1	N.M.....
huMy9-6 V1.2	N.M.....
huMy9-6 V1.3	E.V.....
huMy9-6 V1.4	N.M.....
huMy9-6 V1.5	N.M.....
huMy9-6 V1.6	E.V.....
huMy9-6 V1.7	E.V.....
huMy9-6 V1.8	E.M.....
huMy9-6 V1.9	E.M.....
huMy9-6 V1.10	E.M.....
huMy9-6 V1.11	E.M.....
huMy9-6 V1.12	N.V.....
huMy9-6 V1.13	N.V.....
huMy9-6 V1.14	N.V.....
huMy9-6 V1.15	N.V.....

Kabat #	54	64	74	84	94
muMy9-6	KLLIYWASTR	ESGVPDRFTG	SGSGTDFTLT	ISSVQSEDLA	IYYCHQYLSS
huMy9-6 V1.0	RLLIYWASTR	ESGVPDRFTG	SGSGTDFTLT	ISSVQPEDLA	IYYCHQYLSS
huMy9-6 V1.1	K.....
huMy9-6 V1.2	K.....
huMy9-6 V1.3	R.....
huMy9-6 V1.4	R.....
huMy9-6 V1.5	R.....
huMy9-6 V1.6	K.....
huMy9-6 V1.7	K.....
huMy9-6 V1.8	R.....
huMy9-6 V1.9	R.....
huMy9-6 V1.10	K.....
huMy9-6 V1.11	K.....
huMy9-6 V1.12	R.....
huMy9-6 V1.13	R.....
huMy9-6 V1.14	K.....
huMy9-6 V1.15	K.....

Kabat #	108	
muMy9-6	RTFGGGTKLE	IKR (SEQ ID NO:8)
huMy9-6 V1.0	RTFGQGTKLE	IKR (SEQ ID NO:10)
huMy9-6 V1.1
huMy9-6 V1.2
huMy9-6 V1.3
huMy9-6 V1.4
huMy9-6 V1.5
huMy9-6 V1.6
huMy9-6 V1.7
huMy9-6 V1.8
huMy9-6 V1.9
huMy9-6 V1.10
huMy9-6 V1.11
huMy9-6 V1.12
huMy9-6 V1.13
huMy9-6 V1.14
huMy9-6 V1.15

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Figure 16B

Humanized My9-6 Heavy Chain Versions

Kabat #	10	20	30	40	50
muMy9-6	QVQLQQPGAE	VVKPGASVKM	SCKASGYTFT	SYIHWIKQT	PGQGLEWVG
huMy9-6 V1.0	QVQLQQPGAE	VVKPGASVKM	SCKASGYTFT	SYIHWIKQT	PGQGLEWVG
huMy9-6 V1.1
huMy9-6 V1.2
huMy9-6 V1.3
huMy9-6 V1.4
huMy9-6 V1.5
huMy9-6 V1.6
huMy9-6 V1.7
huMy9-6 V1.8
huMy9-6 V1.9
huMy9-6 V1.10
huMy9-6 V1.11
huMy9-6 V1.12
huMy9-6 V1.13
huMy9-6 V1.14
huMy9-6 V1.15

Kabat #	59	69	79	86	96
muMy9-6	IYPGNDDISY	NQKF K GKATL	TADKSSTTAY	QLSSLTSED	SAVYYCAREV
huMy9-6 V1.0	IYPGNDDISY	NQKF Q GKATL	TADKSSTTAY	QLSSLTSED	SAVYYCAREV
huMy9-6 V1.1K.....
huMy9-6 V1.2Q.....
huMy9-6 V1.3K.....
huMy9-6 V1.4Q.....
huMy9-6 V1.5K.....
huMy9-6 V1.6Q.....
huMy9-6 V1.7K.....
huMy9-6 V1.8Q.....
huMy9-6 V1.9K.....
huMy9-6 V1.10Q.....
huMy9-6 V1.11K.....
huMy9-6 V1.12Q.....
huMy9-6 V1.13K.....
huMy9-6 V1.14Q.....
huMy9-6 V1.15K.....

Kabat #	105	112	
muMy9-6	RLRYFDVWGA	GTTVTVSS	(SEQ ID NO:7)
huMy9-6 V1.0	RLRYFDVW <u>G</u>	GTTVTVSS	(SEQ ID NO:9)
huMy9-6 V1.1	
huMy9-6 V1.2	
huMy9-6 V1.3	
huMy9-6 V1.4	
huMy9-6 V1.5	
huMy9-6 V1.6	
huMy9-6 V1.7	
huMy9-6 V1.8	
huMy9-6 V1.9	
huMy9-6 V1.10	
huMy9-6 V1.11	
huMy9-6 V1.12	
huMy9-6 V1.13	
huMy9-6 V1.14	
huMy9-6 V1.15	

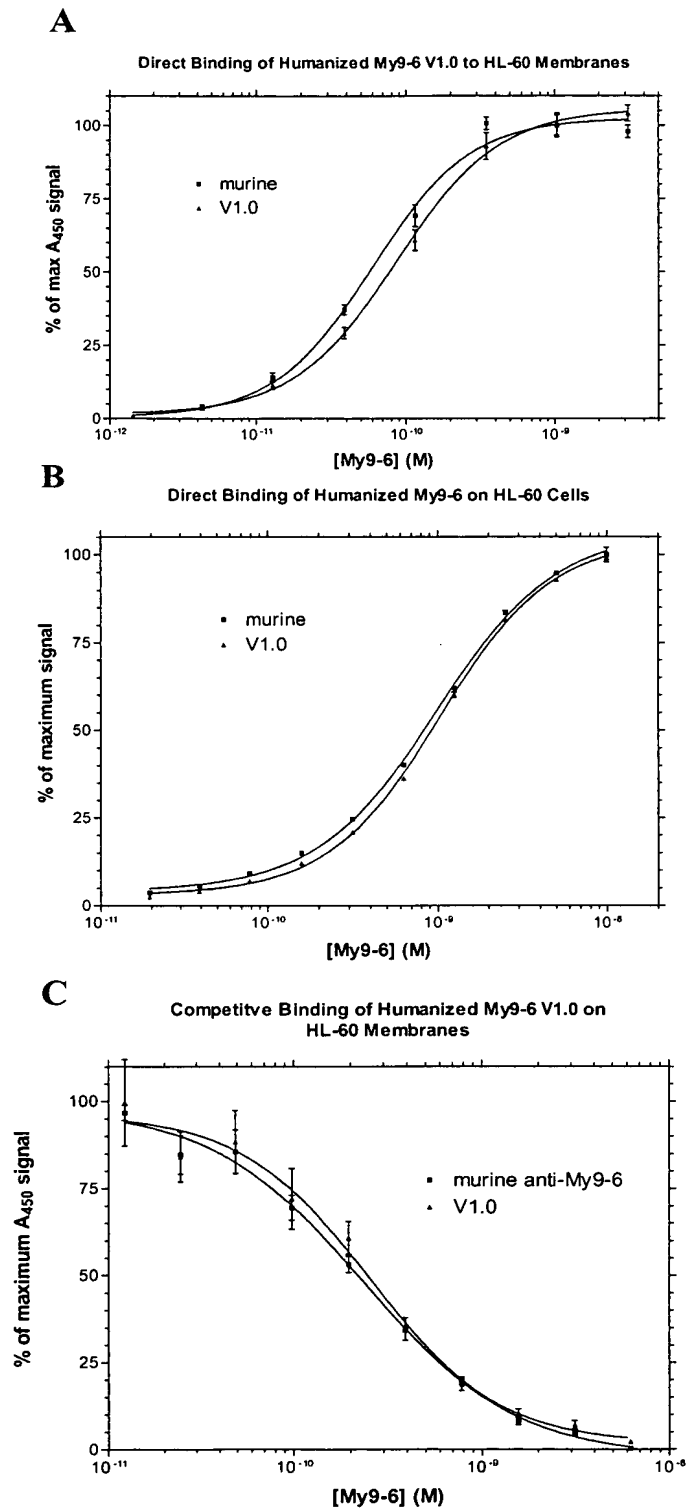
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Figure 17

My9-6 K_D Values			
	Direct on Membranes	Competitive on Membranes	Direct on Cells
	pM	pM	nM
murine	51.34+/-8.74	173.64+/-39.29	1.10+/-0.13
V1.0	66.53+/-17.83	209.00+/-52.37	1.02+/-0.04
V1.1	83.57+/-13.82	279.50+/-152.03*	1.07+/-0.11*
V1.3	63.95+/-0.64*	203.05+/-153.83*	1.16+/-0.39*
V1.6	56.10+/-15.13*	216.50+/-70.00*	0.97+/-0.08*

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Figure 18



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Figure 19

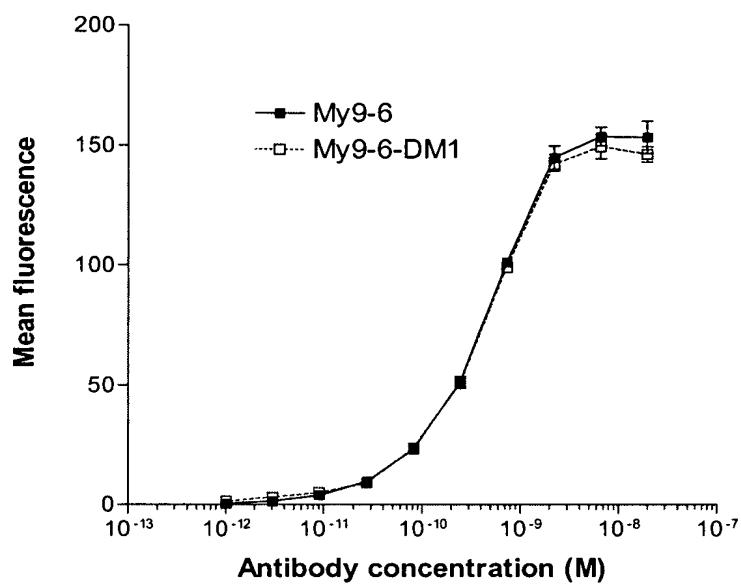
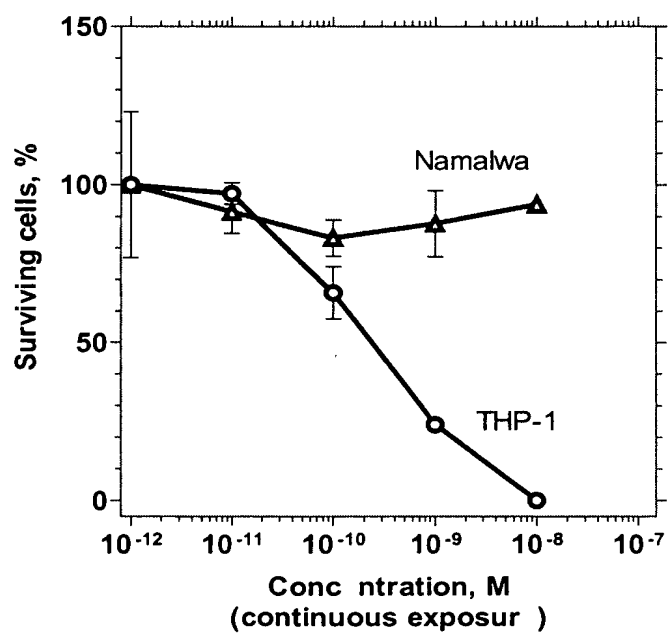
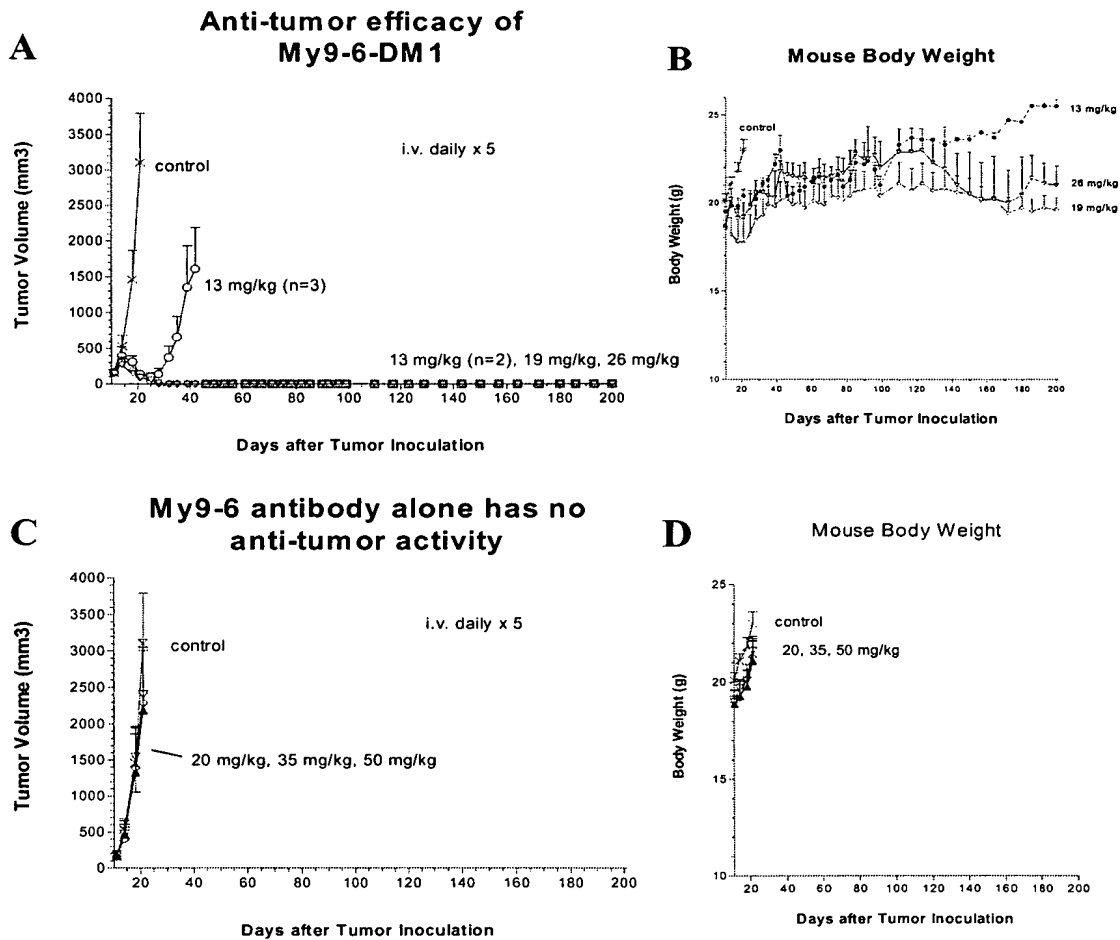


Figure 20



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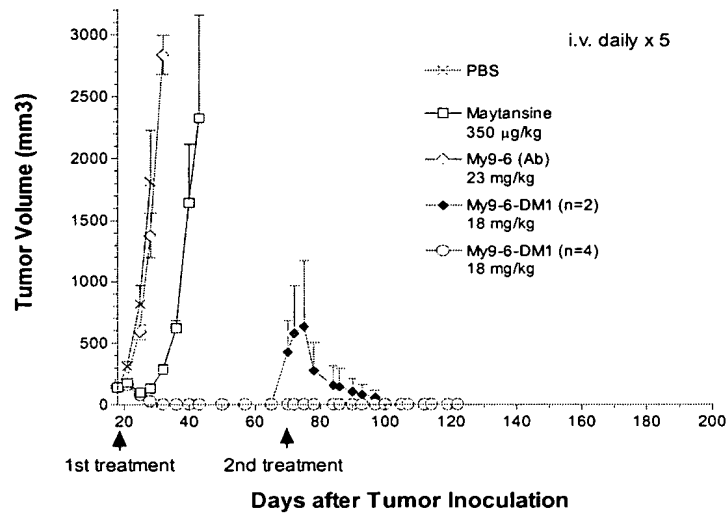
Figure 21



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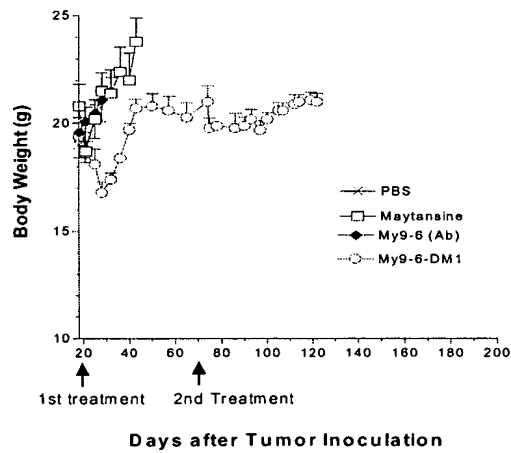
Figure 22

A



B

Mouse Body Weight



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Figure 23A

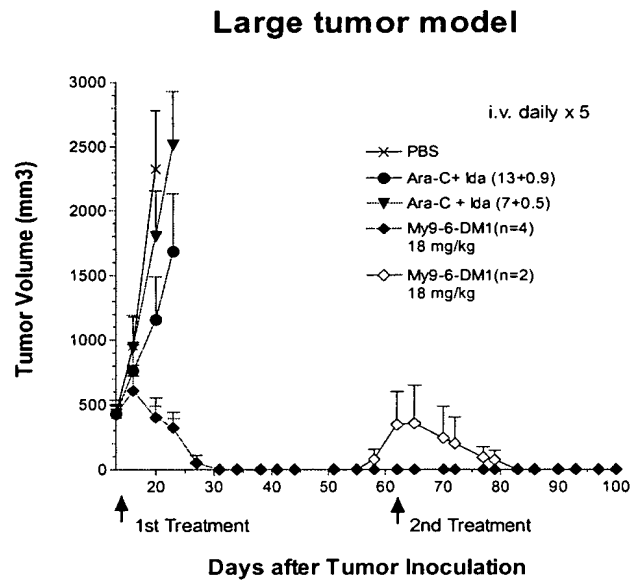


Figure 23B

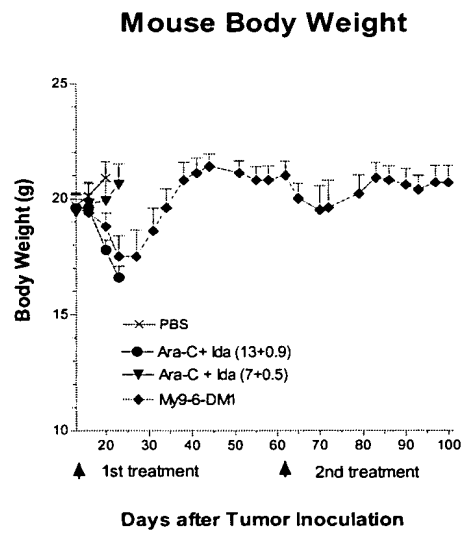


Figure 24A

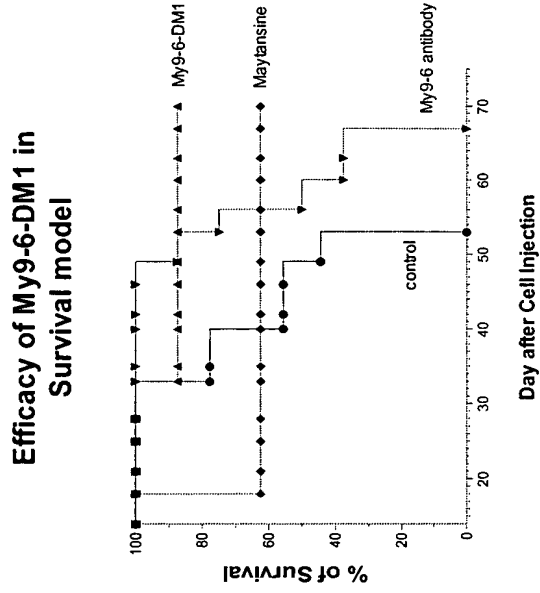


Figure 24B

